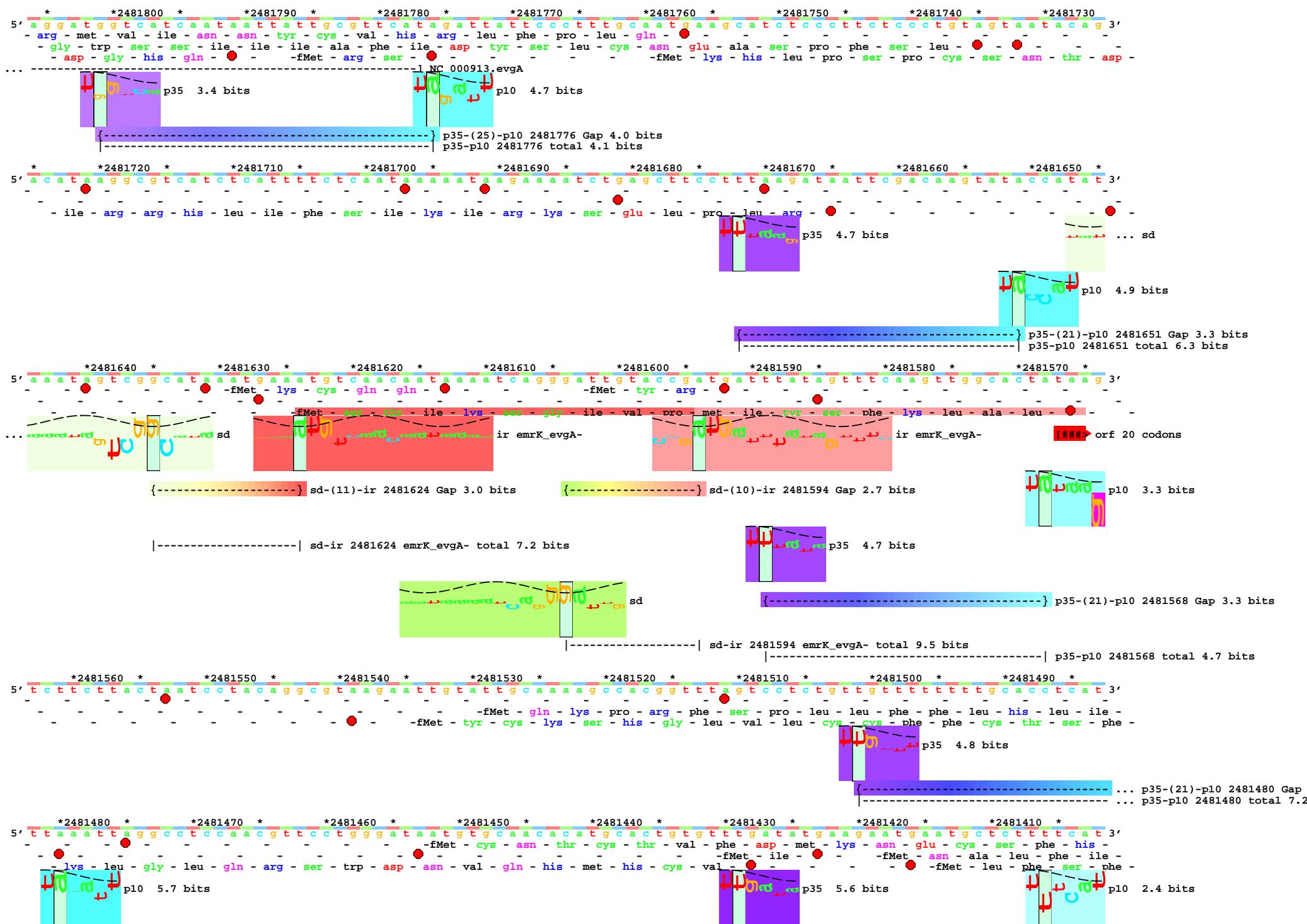


- 1 -  
piece 1, NC\_000913, emrK\_evgA-, config: linear, direction: -, begin: 2481806, end: 2481342



```
... ----} p35-(21)-p10 2481480 Gap 3.3 bits  
... ----| p35-p10 2481480 total 7.2 bits
```

{ p35-(23)-p10 2481406 Gap 1.4 bits  
p35-p10 2481406 total 6.6 bits  
... p10

{ p35-(24)-p10 2481405 Gap 2.4 bits  
p35-p10 2481405 total 4.3 bits  
... p10

{ ... p35-(23)-p10 2481401 Gap 1.4 bits  
... p35-p10 2481401 total 6.6 bits  
... p35-(25)-p10 2481392 Gap 1.4 bits  
... p35-p10 2481392 total 6.6 bits

This diagram illustrates a bacterial operon structure across seven genes. The genes are labeled with their start positions: \*2481400, \*2481390, \*2481380, \*2481370, \*2481360, \*2481350, and ... NC\_000913.emrK. Each gene's reading frame is indicated by a colored bar below its sequence. The sequence is oriented 5' to 3' from left to right. Red dots above the sequence indicate stop codons. Below the genes, several regions are highlighted with colored boxes: a green box labeled 'sd' (sigma factor binding site) and 'p10 5.7 bits'; a red box labeled 'ir emrK\_evG-A' and 'orf 9 codons'; and a yellow box labeled 'sd-(5)-ir 2481374 Gap 5.4 bits'. A blue box at the bottom is labeled 'p10 1.2 bits'. The diagram also shows transcription start sites as arrows pointing downwards.

Diagram illustrating two sequence contexts:

- p35**: 5.3 bits
- sd-(11)-ir**: 2481361 Gap 3.0 bits

The diagram shows a dashed black line above each context, likely representing a signal or promoter element. Below each context is a color bar ranging from green to red, with a bracket indicating the sequence length.

... } p35-(23)-p10 2481401 Gap 1.4 bits

... | p35-p10 2481401 total 4.0 bits

... ----- } p35-(25)-p10 2481392 Gap 4.0 bits

... -----| p35-p10 2481392 total 5.2 bits

```
{-----| p35-(24)-p10 2481364 Gap 2.4 bits  
|-----| p35-p10 2481364 total 5.0 bits
```